

SEQUENCE LISTING

<110> NIPPON SHOKUBAI CO., LTD.

NATIONAL INSTITUTE OF TECHNOLOGY AND EVALUATION

<120> Novel Modified S-Hydroxynitrile lyase

<130> PH-2387-PCT

<140>

<141>

<150> JP 2004-105642

<151> 2004-03-31

<160> 44

<170> PatentIn Ver. 2.1

<210> 1

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<223> Inventor: Ichige, Eita; Semba, Hisashi; Shijuku, Toshiaki; Harayama, Shigeaki

<220>

<221> CDS

<222> (1)..(777)

<400> 1

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

tac gct taa

777

Tyr Ala

<210> 2

<211> 258

<212> PRT

<213> Manihot esculenta

<400> 2

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1

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Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20

25

30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35

40

45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala

<210> 3

<211> 774

<212> DNA

<213> Hevea brasiliensis

<220>

<221> CDS

<222> (1)..(774)

<400> 3

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Met Ala Phe Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

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15

tgg att tgg cac aag ctc aaa ccc ctc ctt gag gca ctt ggc cac aag 96

Trp Ile Trp His Lys Leu Lys Pro Leu Leu Glu Ala Leu Gly His Lys

20

25

30

gtt act gca ctg gac ctt gca gca agc ggc gtt gac cca agg caa att 144

Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Val Asp Pro Arg Gln Ile

35

40

45

gag gag att ggc tca ttt gat gag tat tct gaa ccc ttg ttg acg ttc 192

Glu Glu Ile Gly Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

ttg gag gca ctc cct cca ggg gaa aag gtg att ctg gtt ggc gag agc 240

Leu Glu Ala Leu Pro Pro Gly Glu Lys Val Ile Leu Val Gly Glu Ser

65

70

75

80

tgt gga gga ctc aat ata gca att gct gct gat aaa tac tgt gaa aag 288

Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Cys Glu Lys

85

90

95



att gca gct gct gtt ttc cac aat tca gta ttg cca gac acc gag cac 336

Ile Ala Ala Ala Val Phe His Asn Ser Val Leu Pro Asp Thr Glu His

100

105

110

tgc cca tct tac gtc gtg gat aag ctc atg gag gtg ttt ccc gac tgg 384

Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp

115

120

125

aaa gac acc acg tat ttt acg tac act aaa gat ggc aag gag ata act 432

Lys Asp Thr Thr Tyr Phe Thr Tyr Thr Lys Asp Gly Lys Glu Ile Thr

130

135

140

gga ttg aaa ctg ggc ttc acg ctt ctg agg gaa aat tta tat acc ctt 480

Gly Leu Lys Leu Gly Phe Thr Leu Leu Arg Glu Asn Leu Tyr Thr Leu

145

150

155

160

tgc ggt cct gag gaa tat gaa ctg gcg aag atg ttg aca agg aag gga 528

Cys Gly Pro Glu Glu Tyr Glu Leu Ala Lys Met Leu Thr Arg Lys Gly

165

170

175

tca tta ttt caa aat att tta gct aag cga cca ttc ttc act aag gaa 576

Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu

180

185

190

ggt tac gga tcg att aag aaa att tat gtg tgg acc gac caa gac gaa 624

Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu

195

200

205

ata ttt tta cct gaa ttt caa ctc tgg caa ata gaa aac tat aaa cca 672

Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro

210

215

220

gac aag gtt tat aag gtc gaa ggt gga gat cat aaa ttg cag ctt aca 720

Asp Lys Val Tyr Lys Val Glu Gly Gly Asp His Lys Leu Gln Leu Thr

225

230

235

240

aag act aag gag atc gct gaa att ctc caa gag gtg gct gat acc tat 768

Lys Thr Lys Glu Ile Ala Glu Ile Leu Gln Glu Val Ala Asp Thr Tyr

245

250

255

aat tga

774

Asn

<210> 4

<211> 257

<212> PRT

<213> Hevea brasiliensis

<400> 4

Met Ala Phe Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Leu Leu Glu Ala Leu Gly His Lys

20 25 30

Val Thr Ala Leu Asp Leu Ala Ala Ser Gly Val Asp Pro Arg Gln Ile

35 40 45

Glu Glu Ile Gly Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

Leu Glu Ala Leu Pro Pro Gly Glu Lys Val Ile Leu Val Gly Glu Ser

65 70 75 80

Cys Gly Gly Leu Asn Ile Ala Ile Ala Ala Asp Lys Tyr Cys Glu Lys

85 90 95

Ile Ala Ala Ala Val Phe His Asn Ser Val Leu Pro Asp Thr Glu His

100 105 110

Cys Pro Ser Tyr Val Val Asp Lys Leu Met Glu Val Phe Pro Asp Trp

115 120 125

Lys Asp Thr Thr Tyr Phe Thr Tyr Thr Lys Asp Gly Lys Glu Ile Thr

130

135

140

Gly Leu Lys Leu Gly Phe Thr Leu Leu Arg Glu Asn Leu Tyr Thr Leu

145

150

155

160

Cys Gly Pro Glu Glu Tyr Glu Leu Ala Lys Met Leu Thr Arg Lys Gly

165

170

175

Ser Leu Phe Gln Asn Ile Leu Ala Lys Arg Pro Phe Phe Thr Lys Glu

180

185

190

Gly Tyr Gly Ser Ile Lys Lys Ile Tyr Val Trp Thr Asp Gln Asp Glu

195

200

205

Ile Phe Leu Pro Glu Phe Gln Leu Trp Gln Ile Glu Asn Tyr Lys Pro

210

215

220

Asp Lys Val Tyr Lys Val Glu Gly Gly Asp His Lys Leu Gln Leu Thr

225

230

235

240

Lys Thr Lys Glu Ile Ala Glu Ile Leu Gln Glu Val Ala Asp Thr Tyr

245

250

255

Asn

<210> 5

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<223> cDNA coding for Modified SHNL involving  
a replacement of Gly by Asp at position 165

<220>

<221> CDS

<222> (1)..(777)

<400> 5

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45  
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60  
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110  
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

aaa tgc act gat gac gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528

Lys Cys Thr Asp Asp Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

tac gct taa

777

Tyr Ala

<210> 6

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Gly by Asp at position 165



<400> 6

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145 150 155 160

Lys Cys Thr Asp Asp Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala

<210> 7

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

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<223> cDNA coding for Modified SHNL involving  
a replacement of Gly by Glu at position 165

<400> 7

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145 150 155 160

aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528

Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

tac gct taa

777

Tyr Ala

<210> 8

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Gly by Glu at position 165

<400> 8

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1

5

10

15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20

25

30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35

40

45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

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230

235

240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala

<210> 9

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 9

ggggaattca tggttactgc acacttcggt ctgattcac

39



<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 10

gggaagcttt taagcgtatg catcagcaac ttcttcag

39

<210> 11

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 11

gggggggggc atatggttac tgcacacttc gttctgattc acac

44

<210> 12

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 12

gggggatcct taagcgatg catcagcaac ttctgcag

39

<210> 13

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 13

cgtgaaaacc tggtcaccaa atgcactgat gaagaatatg aactggcaaa aatg 54

<210> 14

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 14

catttttgcc agttcatatt cttcatcagt gcatttggtg aacaggtttt cacg 54

<210> 15

<211> 777

<212> DNA

<213> Manihot esculenta

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<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving

a replacement of Val by Leu at position 173

<400> 15

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg ctg atg cgc aag 528

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys

165

170

175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

tac gct taa

777

Tyr Ala

<210> 16

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Val by Leu at position 173

<400> 16

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145 150 155 160

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys

165 170 175



Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala

<210> 17

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 17

ggcgaatatg aactggcaaa aatgnnnatg cgcaagggct ctctg

45

<210> 18

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 18

cagagagccc ttgcgcatnn ncatttttgc cagttcatat tcgcc

45

<210> 19

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving

a replacement of Met by Leu at position 174

<400> 19

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50	55	60	
ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc    240			
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser			
65	70	75	80
tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa    288			
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys			
	85	90	95
att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac    336			
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His			
100	105	110	
agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg    384			
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp			
115	120	125	
cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc    432			
Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile			
130	135	140	

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145 150 155 160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt ttg cgc aag 528

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Leu Arg Lys

165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

tac gct taa

777

Tyr Ala

<210> 20

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Met by Leu at position 174

<400> 20

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1

5

10

15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20

25

30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35

40

45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Leu Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala

<210> 21

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>



<223> cDNA coding for Modified SHNL(SHNL Actmt022-G12) involving  
a replacement of Lys by Asn at position 21

<400> 21

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aat ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145 150 155 160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

tac gct taa

777

Tyr Ala

<210> 22

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL(SHNL Actmt022-G12) involving

a replacement of Lys by Asn at position 21

<400> 22

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1

5

10

15

Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20

25

30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35

40

45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala

<210> 23

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 23

ggcgcatgga ttggcacnn nctgaaaccg gccctggaa

39

<210> 24

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 24

ttccagggcc ggtttcagnn ngtgccaaat ccatgcgcc

39

<210> 25

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving

a replacement of Lys by Glu at position 21

<400> 25

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac gaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Glu Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80



tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

tac gct taa

777

Tyr Ala

<210> 26

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Lys by Glu at position 21

<400> 26

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

Trp Ile Trp His Glu Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145 150 155 160

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165 170 175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180 185 190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195 200 205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210 215 220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225 230 235 240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala

<210> 27

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving

a replacement of Lys by Asp at position 21

<400> 27

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1

5

10

15

tgg att tgg cac gac ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Asp Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20

25

30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35

40

45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

tac gct taa

777

Tyr Ala



<210> 28

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Lys by Asp at position 21

<400> 28

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

Trp Ile Trp His Asp Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala

<210> 29

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving

a replacement of Lys by Asn at position 21

<400> 29

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aac ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20

25

30

ggt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35

40

45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

aaa tgc act gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

tac gct taa

777

Tyr Ala

<210> 30

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Lys by Asn at position 21

<400> 30

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

Trp Ile Trp His Asn Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

Lys Cys Thr Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala

<210> 31

<211> 777



<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving

replacement of Gly by Glu at position 165 and Val by Leu at position 173

<400> 31

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45  
gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192  
Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240  
Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288  
Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336  
Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384  
Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg ctg atg cgc aag 528

Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys

165

170

175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

tac gct taa

777

Tyr Ala

<210> 32

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

replacement of Gly by Glu at position 165 and Val by Leu at position 173

<400> 32

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145 150 155 160

Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Met Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala

<210> 33

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 33

tatgaactgg caaaaatgct gctgcgcaag ggctctctgt tc

42

<210> 34

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 34

gaacagagag cccttgcgca gcagcatttt tgccagtta ta

42

<210> 35

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<221> CDS

<222> (1)..(777)

<220>

<223> cDNA coding for Modified SHNL involving

replacement of Gly by Glu at position 165 and Val by Leu at position 173 and  
Met by Leu at position 174

<400> 35

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45



gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

aaa tgc act gat gaa gaa tat gaa ctg gca aaa atg ctg ctg cgc aag 528

Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Leu Arg Lys

165

170

175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

tac gct taa

777

Tyr Ala

<210> 36

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

replacement of Gly by Glu at position 165 and Val by Leu at position 173 and

Met by Leu at position 174

<400> 36

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115 120 125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130 135 140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145 150 155 160

Lys Cys Thr Asp Glu Glu Tyr Glu Leu Ala Lys Met Leu Leu Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 37

tgaaaacctg ttcaccaa at gcnngatgg cgaatatgaa ctggc

45

<210> 38

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 38

gccagttcat attcgccatc nnngcatttg gtgaacaggt ttca

45

<210> 39

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<223> cDNA coding for Modified SHNL involving  
a replacement of Thr by Asp at position 163

<220>

<221> CDS

<222> (1)..(777)

<223>

<400> 39

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile



130	135	140	
act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc			480
Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr			
145	150	155	160
aaa tgc gat gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag			528
Lys Cys Asp Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys			
	165	170	175
ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa			576
Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu			
	180	185	190
aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac			624
Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp			
195	200	205	
aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa			672
Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys			
210	215	220	

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225 230 235 240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245 250 255

tac gct taa 777

Tyr Ala

<210> 40

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Thr by Asp at position 163

<400> 40

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

Lys Cys Asp Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala

<210> 41

<211> 777

<212> DNA

<213> Manihot esculenta

<220>

<223> cDNA coding for Modified SHNL involving  
a replacement of Thr by Glu at position 163

<220>

<221> CDS

<222> (1)..(777)

<223>

<400> 41

atg gtt act gca cac ttc gtt ctg att cac acc att tgt cac ggc gca 48

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1

5

10

15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20

25

30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35

40

45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

aaa tgc gaa gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528

Lys Cys Glu Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190



aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

tac gct taa

777

Tyr Ala

<210> 42

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Thr by Glu at position 163

<400> 42

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1

5

10

15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20

25

30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35

40

45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

Lys Cys Glu Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

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Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

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250

255

Tyr Ala

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<211> 777

<212> DNA

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a replacement of Thr by Ser at position 163

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<221> CDS

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Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

1 5 10 15

tgg att tgg cac aaa ctg aaa ccg gcc ctg gaa cgt gct ggc cac aaa 96

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20 25 30

gtt act gca ctg gac atg gca gcc agt ggc att gac ccg cgt caa att 144

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35 40 45

gaa cag atc aac tct ttc gat gaa tac tct gaa ccg ctg ctg act ttc 192

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50 55 60

ctg gaa aaa ctg ccg caa ggc gaa aag gtt atc att gtt ggt gaa agc 240

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65 70 75 80

tgt gca ggc ctg aac att gct att gct gct gat cgt tac gtt gac aaa 288

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85 90 95

att gca gct ggc gtt ttc cac aac tcc ctg ctg ccg gac acc gtt cac 336

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100 105 110

agc ccg tct tac act gtt gaa aag ctg ctg gaa tcg ttc ccg gac tgg 384

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115 120 125

cgt gac aca gaa tat ttc acg ttc acc aac atc act ggc gaa acc atc 432

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130 135 140

act acc atg aaa ctg ggt ttc gtt ctg ctg cgt gaa aac ctg ttc acc 480

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145 150 155 160

aaa tgc tct gat ggc gaa tat gaa ctg gca aaa atg gtt atg cgc aag 528

Lys Cys Ser Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165 170 175

ggc tct ctg ttc caa aac gtt ctg gct cag cgt ccg aag ttc act gaa 576

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180 185 190

aaa ggc tac ggc tct atc aag aaa gtt tat att tgg acc gat caa gac 624

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195 200 205

aaa ata ttc ctg ccg gac ttc caa cgc tgg caa att gca aac tac aaa 672

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210 215 220

ccg gac aag gtt tat cag gtt caa ggc ggc gat cac aag ctg cag ctg 720

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225 230 235 240



aca aaa act gaa gaa gta gct cac att ctg caa gaa gtt gct gat gca 768

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

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255

tac gct taa

777

Tyr Ala

<210> 44

<211> 258

<212> PRT

<213> Manihot esculenta

<220>

<223> Modified SHNL involving

a replacement of Thr by Ser at position 163

<400> 44

Met Val Thr Ala His Phe Val Leu Ile His Thr Ile Cys His Gly Ala

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5

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15

Trp Ile Trp His Lys Leu Lys Pro Ala Leu Glu Arg Ala Gly His Lys

20

25

30

Val Thr Ala Leu Asp Met Ala Ala Ser Gly Ile Asp Pro Arg Gln Ile

35

40

45

Glu Gln Ile Asn Ser Phe Asp Glu Tyr Ser Glu Pro Leu Leu Thr Phe

50

55

60

Leu Glu Lys Leu Pro Gln Gly Glu Lys Val Ile Ile Val Gly Glu Ser

65

70

75

80

Cys Ala Gly Leu Asn Ile Ala Ile Ala Ala Asp Arg Tyr Val Asp Lys

85

90

95

Ile Ala Ala Gly Val Phe His Asn Ser Leu Leu Pro Asp Thr Val His

100

105

110

Ser Pro Ser Tyr Thr Val Glu Lys Leu Leu Glu Ser Phe Pro Asp Trp

115

120

125

Arg Asp Thr Glu Tyr Phe Thr Phe Thr Asn Ile Thr Gly Glu Thr Ile

130

135

140

Thr Thr Met Lys Leu Gly Phe Val Leu Leu Arg Glu Asn Leu Phe Thr

145

150

155

160

Lys Cys Ser Asp Gly Glu Tyr Glu Leu Ala Lys Met Val Met Arg Lys

165

170

175

Gly Ser Leu Phe Gln Asn Val Leu Ala Gln Arg Pro Lys Phe Thr Glu

180

185

190

Lys Gly Tyr Gly Ser Ile Lys Lys Val Tyr Ile Trp Thr Asp Gln Asp

195

200

205

Lys Ile Phe Leu Pro Asp Phe Gln Arg Trp Gln Ile Ala Asn Tyr Lys

210

215

220

Pro Asp Lys Val Tyr Gln Val Gln Gly Gly Asp His Lys Leu Gln Leu

225

230

235

240

Thr Lys Thr Glu Glu Val Ala His Ile Leu Gln Glu Val Ala Asp Ala

245

250

255

Tyr Ala